#2

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/017,393

DATE: 01/03/2002
TIME: 13:39:45

Input Set : A:\16U 103 R1.ST25.txt
Output Set: N:\CRF3\01032002\J017393.raw

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  3 <110> APPLICANT: OriGene Technologies, Inc
  5 <120> TITLE OF INVENTION: HISTAMINE H2 RECEPTOR AND USES
  7 <130> FILE REFERENCE: 16U 103 R1
  9 <140> CURRENT APPLICATION NUMBER: US/10/017,393
  9 <141> CURRENT FILING DATE: 2001-12-18
  9 <160> NUMBER OF SEQ ID NOS: 2
 11 <170> SOFTWARE: PatentIn version 3.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 4175
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Homo sapiens
 18 <220> FEATURE:
 19 <221> NAME/KEY: CDS
 20 <222> LOCATION: (103)..(1371)
 21 <223> OTHER INFORMATION:
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 27 accaggggcc ctgatcaggg gactgagccg tagagtccca gg atg gca ccc aat      114
 28                                                 Met Ala Pro Asn
 29                                                 1
 31 ggc aca gcc tct tcc ttt tgc ctg gac tct acc gca tgc aag atc acc      162
 32 Gly Thr Ala Ser Ser Phe Cys Leu Asp Ser Thr Ala Cys Lys Ile Thr
 33 5                   10                  15                  20
 35 atc acc gtg gtc ctt gcg gtc ctc atc ctc atc acc gtt gct ggc aat      210
 36 Ile Thr Val Val Leu Ala Val Leu Ile Leu Ile Thr Val Ala Gly Asn
 37                  25                  30                  35
 39 gtg gtc gtc tgt ctg gcc gtg ggc ttg aac cgc cgg ctc cgc aac ctg      258
 40 Val Val Val Cys Leu Ala Val Gly Leu Asn Arg Arg Leu Arg Asn Leu
 41              40                  45                  50
 43 acc aat tgt ttc atc gtg tcc ttg gct atc act gac ctg ctc ctc ggc      306
 44 Thr Asn Cys Phe Ile Val Ser Leu Ala Ile Thr Asp Leu Leu Leu Gly
 45          55                  60                  65
 47 ctc ctg gtg ctg ccc ttc tct gcc atc tac cag ctg tcc tgc aag tgg      354
 48 Leu Leu Val Leu Pro Phe Ser Ala Ile Tyr Gln Leu Ser Cys Lys Trp
 49      70                  75                  80
 51 agc ttt ggc aag gtc ttc tgc aat atc tac acc agc ctg gat gtg atg      402
 52 Ser Phe Gly Lys Val Phe Cys Asn Ile Tyr Thr Ser Leu Asp Val Met
 53 85                  90                  95                  100
 55 ctc tgc aca gcc tcc att ctt aac ctc ttc atg atc agc ctc gac cgg      450
 56 Leu Cys Thr Ala Ser Ile Leu Asn Leu Phe Met Ile Ser Leu Asp Arg
 57                 105                 110                 115
 59 tac tgc gct gtc atg gac cca ctg cgg tac cct gtg ctg gtc acc cca      498
 60 Tyr Cys Ala Val Met Asp Pro Leu Arg Tyr Pro Val Leu Val Thr Pro
 61             120                 125                 130
 63 gtt cgg gtc gcc atc tct ctg gtc tta att tgg gtc atc tcc att acc      546
 64 Val Arg Val Ala Ile Ser Leu Val Leu Ile Trp Val Ile Ser Ile Thr
 65         135                 140                 145
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67 ctg tcc ttt ctg tct atc cac ctg ggg tgg aac agc agg aac gag acc      594
68 Leu Ser Phe Leu Ser Ile His Leu Gly Trp Asn Ser Arg Asn Glu Thr
69     150                 155                 160
71 agc aag ggc aat cat acc acc tct aag tgc aaa gtc cag gtc aat gaa      642
72 Ser Lys Gly Asn His Thr Thr Ser Lys Cys Lys Val Gln Val Asn Glu
73 165                 170                 175                 180
75 gtg tac ggg ctg gtg gat ggg ctg gtc acc ttc tac ctc ccg cta ctg      690
76 Val Tyr Gly Leu Val Asp Gly Leu Val Thr Phe Tyr Leu Pro Leu Leu
77                 185                 190                 195
79 atc atg tgc atc acc tac tac cgc atc ttc aag gtc gcc cgg gat cag      738
80 Ile Met Cys Ile Thr Tyr Tyr Arg Ile Phe Lys Val Ala Arg Asp Gln
81             200                 205                 210
83 gcc aag agg atc aat cac att agc tcc tgg aag gca gcc acc atc agg      786
84 Ala Lys Arg Ile Asn His Ile Ser Ser Trp Lys Ala Ala Thr Ile Arg
85         215                 220                 225
87 gag cac aaa gcc aca gtg aca ctg gcc gcc gtc atg ggg gcc ttc atc      834
88 Glu His Lys Ala Thr Val Thr Leu Ala Ala Val Met Gly Ala Phe Ile
89     230                 235                 240
91 atc tgc tgg ttt ccc tac ttc acc gcg ttt gtg tac cgt ggg ctg aga      882
92 Ile Cys Trp Phe Pro Tyr Phe Thr Ala Phe Val Tyr Arg Gly Leu Arg
93 245                 250                 255                 260
95 ggg gat gat gcc atc aat gag gtg tta gaa gcc atc gtt ctg tgg ctg      930
96 Gly Asp Asp Ala Ile Asn Glu Val Leu Glu Ala Ile Val Leu Trp Leu
97                 265                 270                 275
99 ggc tat gcc aac tca gcc ctg aac ccc atc ctg tat gct gcg ctg aac      978
100 Gly Tyr Ala Asn Ser Ala Leu Asn Pro Ile Leu Tyr Ala Ala Leu Asn
101             280                 285                 290
103 aga gac ttc cgc acc ggg tac caa cag ctc ttc tgc tgc agg ctg gcc     1026
104 Arg Asp Phe Arg Thr Gly Tyr Gln Gln Leu Phe Cys Cys Arg Leu Ala
105         295                 300                 305
107 aac cgc aac tcc cac aaa act tct ctg agg tcc aac gcc tct cag ctg     1074
108 Asn Arg Asn Ser His Lys Thr Ser Leu Arg Ser Asn Ala Ser Gln Leu
109     310                 315                 320
111 tcc agg acc caa agc cga gaa ccc agg caa cag gaa gag aaa ccc ctg     1122
112 Ser Arg Thr Gln Ser Arg Glu Pro Arg Gln Gln Glu Glu Lys Pro Leu
113 325                 330                 335                 340
115 aag ctc cag gtg tgg agt ggg aca gaa gtc acg gcc ccc cag gga gcc     1170
116 Lys Leu Gln Val Trp Ser Gly Thr Glu Val Thr Ala Pro Gln Gly Ala
117                 345                 350                 355
119 aca gac agg aag cca gca ctg tcc tgc act acg tgc tcc agc aac ctc     1218
120 Thr Asp Arg Lys Pro Ala Leu Ser Cys Thr Thr Cys Ser Ser Asn Leu
121             360                 365                 370
123 ctg agc tgc tgc aag agc ctg tgg ggg ctc agg ttc ctt cag aga cac     1266
124 Leu Ser Cys Cys Lys Ser Leu Trp Gly Leu Arg Phe Leu Gln Arg His
125         375                 380                 385
127 atg gga ggc ccc tcg gag gag cta tcg ggg gag cca ctg tct gag gag     1314
128 Met Gly Gly Pro Ser Glu Glu Leu Ser Gly Glu Pro Leu Ser Glu Glu
129     390                 395                 400
131 cca cag aag aga cct ccc cag aaa gcg gtg agg acg ctg ccc tct gag     1362
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132 Pro Gln Lys Arg Pro Pro Gln Lys Ala Val Arg Thr Leu Pro Ser Glu
133 405                 410                 415                 420
135 gct gtc tag acctagcccc aggacactga agataccgct cccggtcccc            1411
136 Ala Val
139 aagatgtgac tcctggagct cctaaggacc cagtctccaa agccaccaag gactcaccct   1471
141 ggactgaatc tgggggctcc cagaacacac agctgggtgt ggggtcctca ggcctagggc   1531
143 ggaacagcct attctgtgct cagcattccc agacaggcac gcaagactcc tctgggcccg   1591
145 agtgggctga atcccatggg ttcaaagctc acgttggtgc tggccctggg agtcatgagc   1651
147 agagacggtg ggacagacgg ggatgcgtgc acatgtgtgt gcatgggtgc atacgtgtag   1711
149 ggacgtgcat gacctctgag caaggcagag ggtattgaag aaagcattgg cctctcactc   1771
151 cctcatgggt tctgcaggat gaaggaaagg aaaggaaaag acagagaaag gaaggaaata   1831
153 gcttttcatg agcacctact gtgtaccagg tgcttccctg gcatgagctc tcgtaaccct   1891
155 tatagcaaca tgagtttaga gcaagaatca caccccgact ttacagagat ggaaactgag   1951
157 gctcagagaa gtaagggacc tgcccaaggc cactcagcac ctagaaagtg tgcctagcac   2011
159 ataggaggca cacaaaaata tgtgttgaat gggtgaatga atgagagaac gggtgaaaag   2071
161 ccaggcctca agcccacact actgacactg cactacacca cctctcagga gagaaggcaa   2131
163 atatttcctt gactcagcca ccttcctcct agcaaggctt agacccccag gctctggggg   2191
165 tcccttcctg ctacagtatg accctctctg gtgcttgtca tcaagaagtg gtatgcggtg   2251
167 gacttgctgg agagagtgtc tgcagccagg catcatggag ggagggatgg atcttgaggg   2311
169 actgtaatgg ttgtgaatgg gggagttggc ccccagcact ctctggtggc cgtatgacct   2371
171 tgggcacgtc tcctgaccac tctaagcagc ttttgattcc cctgtccaag agggtaggcc   2431
173 ccctgttcct atttacagga tccataaaga gactcaaaga gatagggtag tgccagcccc   2491
175 agagagaggg ggctgtggag ggacttctac ccccagggct tctcagtggc atctcctggc   2551
177 tggcccctga cactcaatct tccttggttt ccaagatgct tcatgatctt ccccctccct   2611
179 gacatccccg acctcccttt tctgtccctt ttgcaactca ttgtcctcta cctgccatca   2671
181 gatgtggctg ttcctcagtc tcagtccaga gtcctctctt ctcactcagc atctctcctc   2731
183 ctgtgacctc gtctgcaccc acaactccag ttacaaggca cgaggtttgg ttatgaaatc   2791
185 actcacagat ttataactgc aggcttggct ccttccggga gcttgagacc cactgccgcc   2851
187 tccgcaacac ctccacctgg gagtttcaga ggcgctctcc ctcagcgtgt ctgcagctgc   2911
189 gtgcctgcag ctgcgtgcct gccttctccc tgcacctgct ctgctcccca ggtccctttc   2971
191 tcagaccaaa gcctgcccgg gcttcacagg ctgagggtcc accttgccac ctccgtttgc   3031
193 ctcagtcctc atggagccct ggctccactg tctgctggct tctccccatc tactctgtgt   3091
195 cactccatcc gaccaccatt gtctccatca ggacagttgg aacacctctt ctcagcactc   3151
197 tcgcccccac ccagtccacc ccctacctga cagccagagt gggccatgcc agatgcaacc   3211
199 caggtcatgc cacacaggta gataaaacca tcttcagccc agccctcagg ccctgtgtgc   3271
201 tgggaccctg ctgggccctc tccagcctcc ccctgcgcca ggcctcctcc gtcacttcac   3331
203 tctggccctg ctgttctttt ccttttagtt tgattaactc actctgccca ttccatgctc   3391
205 aaagctgttt ccgtgaggaa aggctcctcc tgctcatttt agtgccctga aatgtcactt   3451
207 ccttgaggaa gtcttccttg accctccaca ccaaaccagg ccccctgcca caccctcag   3511
209 agctctcctt ggaaggcact ggcatggctg tttgcgtgat tccttgaacg ttgtctgtct   3571
211 ctcctcctca ccaggctgtg ggtcctgtct gtttctggtg accgttgtct gtctaacccc   3631
213 tagaggagag tttgtcacat ggtaggagct taataaatat gtgttggatg aatgatcaga   3691
215 gaaaagagag tgcagagagt ggccaaaaca gatgctttca gcagtgtatc tgccaataaa   3751
217 cctaaaggca tgatttgccc tggtgatccc cccagaggtg cttagtctct tggctgaatt   3811
219 ccttctggaa tccccagaat ccccctcctt ggaagttttc ccaggagtct gaggcaggca   3871
221 ggtctctcag tcacggccac atgacctcaa gtgaaaacaa accagtctgg ctgttcacag   3931
223 actcagctgg tcagagctct ggcccgaggg gcccacgcac cacccgccac tgcagaagac   3991
225 gcctccacgt ctgtctctgg gctgcctcca ccttctgcag gcctcctgga gcctctgctg   4051
227 gctgcagaag tggggtgcat gctgcctgga ggaggaacat ctgtggtggg accccaaatc   4111
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229 catgtttgtg ttaccatcgt gttccaataa aactatcgaa acagaaaaaa aaaaaaaaaa   4171
231 aaaa                                                               4175
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235 <211> LENGTH: 422
236 <212> TYPE: PRT
237 <213> ORGANISM: Homo sapiens
239 <400> SEQUENCE: 2
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242 1               5                  10                  15
245 Cys Lys Ile Thr Ile Thr Val Val Leu Ala Val Leu Ile Leu Ile Thr
246             20                  25                  30
249 Val Ala Gly Asn Val Val Val Cys Leu Ala Val Gly Leu Asn Arg Arg
250         35                  40                  45
253 Leu Arg Asn Leu Thr Asn Cys Phe Ile Val Ser Leu Ala Ile Thr Asp
254     50                  55                  60
257 Leu Leu Leu Gly Leu Leu Val Leu Pro Phe Ser Ala Ile Tyr Gln Leu
258 65                  70                  75                  80
261 Ser Cys Lys Trp Ser Phe Gly Lys Val Phe Cys Asn Ile Tyr Thr Ser
262                 85                  90                  95
265 Leu Asp Val Met Leu Cys Thr Ala Ser Ile Leu Asn Leu Phe Met Ile
266             100                 105                 110
269 Ser Leu Asp Arg Tyr Cys Ala Val Met Asp Pro Leu Arg Tyr Pro Val
270         115                 120                 125
273 Leu Val Thr Pro Val Arg Val Ala Ile Ser Leu Val Leu Ile Trp Val
274     130                 135                 140
277 Ile Ser Ile Thr Leu Ser Phe Leu Ser Ile His Leu Gly Trp Asn Ser
278 145                 150                 155                 160
281 Arg Asn Glu Thr Ser Lys Gly Asn His Thr Thr Ser Lys Cys Lys Val
282                 165                 170                 175
285 Gln Val Asn Glu Val Tyr Gly Leu Val Asp Gly Leu Val Thr Phe Tyr
286             180                 185                 190
289 Leu Pro Leu Leu Ile Met Cys Ile Thr Tyr Tyr Arg Ile Phe Lys Val
290         195                 200                 205
293 Ala Arg Asp Gln Ala Lys Arg Ile Asn His Ile Ser Ser Trp Lys Ala
294     210                 215                 220
297 Ala Thr Ile Arg Glu His Lys Ala Thr Val Thr Leu Ala Ala Val Met
298 225                 230                 235                 240
301 Gly Ala Phe Ile Ile Cys Trp Phe Pro Tyr Phe Thr Ala Phe Val Tyr
302                 245                 250                 255
305 Arg Gly Leu Arg Gly Asp Asp Ala Ile Asn Glu Val Leu Glu Ala Ile
306             260                 265                 270
309 Val Leu Trp Leu Gly Tyr Ala Asn Ser Ala Leu Asn Pro Ile Leu Tyr
310         275                 280                 285
313 Ala Ala Leu Asn Arg Asp Phe Arg Thr Gly Tyr Gln Gln Leu Phe Cys
314     290                 295                 300
317 Cys Arg Leu Ala Asn Arg Asn Ser His Lys Thr Ser Leu Arg Ser Asn
318 305                 310                 315                 320
321 Ala Ser Gln Leu Ser Arg Thr Gln Ser Arg Glu Pro Arg Gln Gln Glu
322                 325                 330                 335
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```
325 Glu Lys Pro Leu Lys Leu Gln Val Trp Ser Gly Thr Glu Val Thr Ala
326             340                 345                 350
329 Pro Gln Gly Ala Thr Asp Arg Lys Pro Ala Leu Ser Cys Thr Thr Cys
330         355                 360                 365
333 Ser Ser Asn Leu Leu Ser Cys Cys Lys Ser Leu Trp Gly Leu Arg Phe
334     370                 375                 380
337 Leu Gln Arg His Met Gly Gly Pro Ser Glu Glu Leu Ser Gly Glu Pro
338 385                 390                 395                 400
341 Leu Ser Glu Glu Pro Gln Lys Arg Pro Pro Gln Lys Ala Val Arg Thr
342                 405                 410                 415
345 Leu Pro Ser Glu Ala Val
346             420
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/017,393**

DATE: 01/03/2002
TIME: 13:39:46

Input Set : **A:\16U 103 R1.ST25.txt**
Output Set: **N:\CRF3\01032002\J017393.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date